Fig. 1a

Fig. 1b

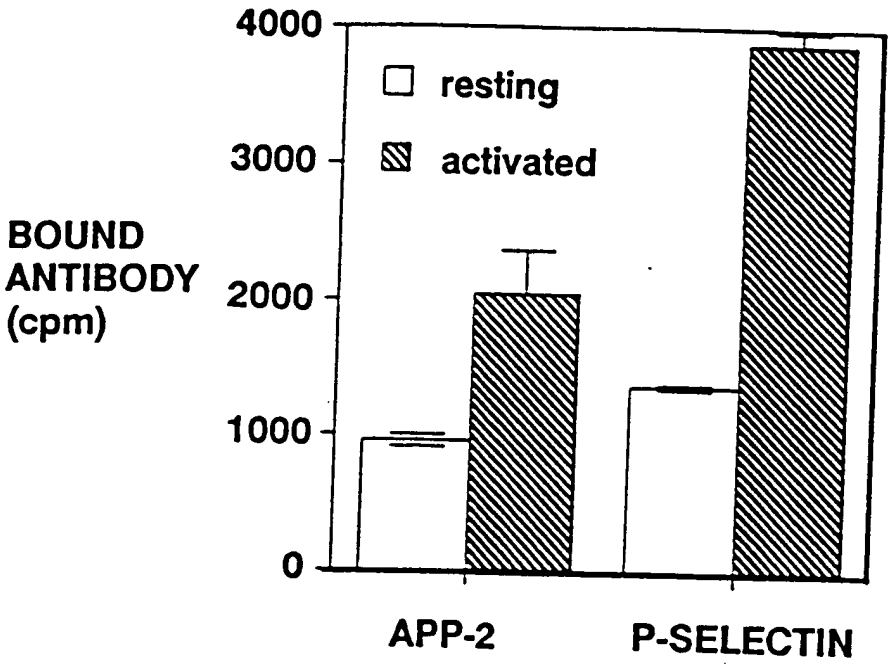
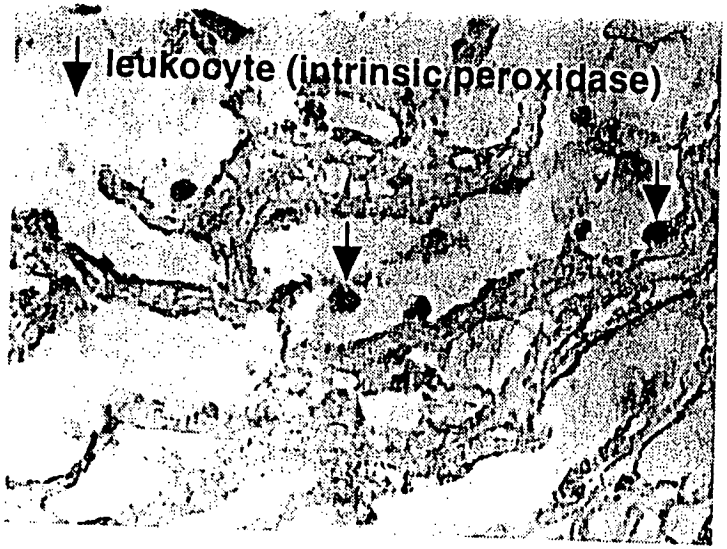
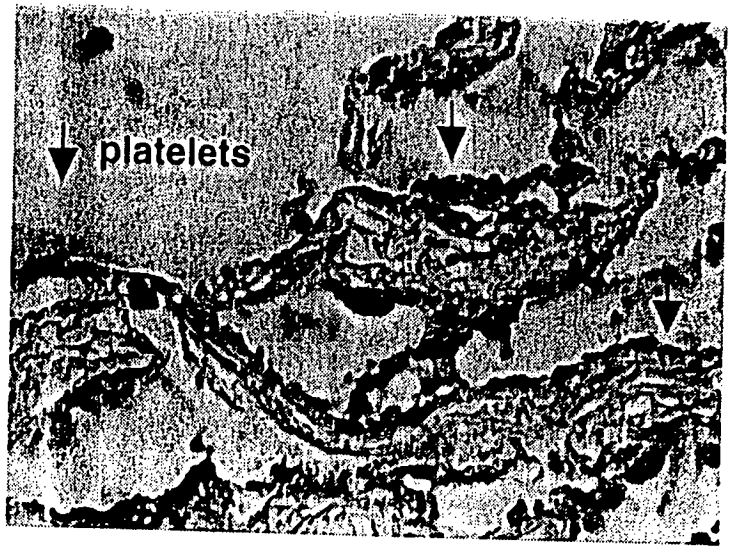

4000
3000
2000
1000
0
resting
activated
BOUND
ANTIBODY
(cpm)
APP-2
P-SELECTIN

Fig. 2

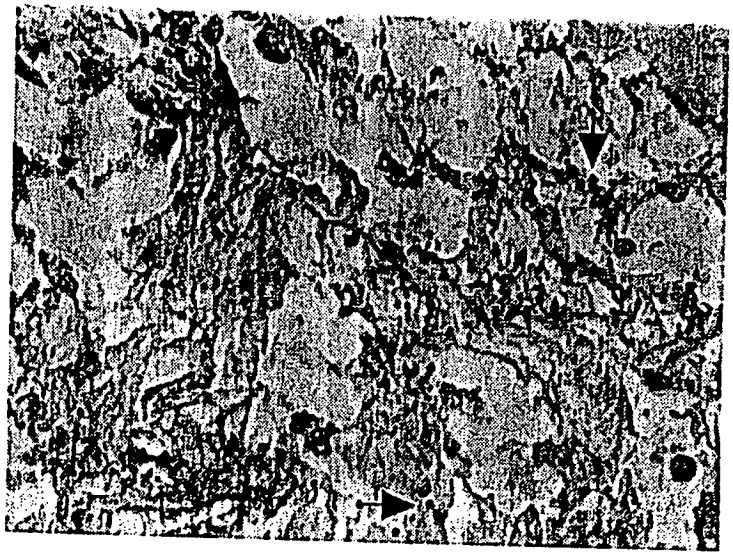
Fig. 3



Control



Anti–
APP-2



Anti–
P-Selectin

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GCACCTGGCG GTGAAGCTGG CTGACCAGCC ACTTACTCCA AAGTCTATTC TTCGGTTGCC     120
AGAGACAGAA CTGGGAGAAT ACTCGCTAGG GGGCTATAGT ATTTCATTTC TGAAGCAGCT     180
TATTGCTGGC AAACTCCAGG AGTCTGTTCC AGACCCTGAG CTGATTGATC TGATCTACTG     240
TGGTCGGAAG CTAAAAGATG ACCAGACACT TGACTTCTAT GGCATTCAAC CTGGGTCCAC     300
TGTCCATGTT CTGCGAAAGT CCTGGCCTGA ACCTGATCAG AAACCGGAAC CTGTGGACAA     360
AGTGGCTGCC ATGAGAGAGT TCCGGGTGTT GCACACTGCC CTGCACAGCA GCTCCTCTTA     420
CAGGGAGGCG GTCTTTAAGA TGCTCAGCAA TAAGGAGTCT CTGGATCAGA TCATTGTGGC     480
CACCCCAGGC CTCAGCAGTG ACCCTATTGC TCTTGGGGTT CTCCAGGACA AGGACCTCTT     540
CTCTGTCTTC GCTGATCCCA ATATGCTTGA TACGTTGGTG CCTGCTCACC CAGCCCTCGT     600
CAATGCCATT GTCCTGGTTC TGCACTCCGT AGCAGGCAGT GCCCCAATGC CTGGGACTGA     660
CTCCTCTTCC CGGAGCATGC CCTCCAGCTC ATACCGGGAT ATGCCAGGTG GCTTCCTGTT     720
TGAAGGGCTC TCAGATGATG AGGATGACTT TCACCCAAAC ACCAGGTCCA CACCCTCTAG     780
CAGTACTCCC AGCTCCCGCC CAGCCTCCCT GGGGTACAGT GGAGCTGCTG GGCCCCGGCC     840
CATCACCCAG AGTGAGCTGG CCACCGCCTT GGCCCTGGCC AGCACTCCGG AGAGCAGCTC     900
TCACACACCG ACTCCTGGCA CCCAGGGTCA TTCCTCAGGG ACCTCACCAA TGTCCTCTGG     960
TGTCCAGTCA GGGACGCCCA TCACCAATGA TCTCTTCAGC CAAGCCCTAC AGCATGCCCT    1020
TCAGGCCTCT GGGCAGCCCA GCCTTCAGAG CCAGTGGCAG CCCCAGCTGC AGCAGCTACG    1080
TGACATGGGC ATCCAGGACG ATGAGCTGAG CCTGCGGCCC TGCAGGCCAC CGGTGGGGAC    1140
ATCCAAGCAG CCCTGGAGCT CATCTTTGCT GGAGGAGCCC CATGAACTCC CTGCTTCCCC    1200
TGAACCCCCA GCAAGTTGCA GAGGCTACTG CCCTTGGGAG GCACTCATGA AGGTGCCTCC    1260
ATCTCTCCCT TCCCCAATAT ACCTGATGGT CAACTCTAAA AAAAAAAAAA AAAAAAAAAA    1320
ATGAAATACC ACTACTCTGA TCGTTTTTTC ACTGACCCGG TGAGGCGGCG CGA           1373
```

Fig. 4

MSLSDWHLAV KLADQPLTPK SILRLPETEL GEYSLGGYSI SFLKQLIAGK LQESVPDPEL 60

IDLIYCGRKL KDDQTLDFYG IQPGSTVHVL RKSWPEPDQK PEPVDKVAAM REFRVLHTAL 120

HSSSSYREAV FKMLSNKESL DQIIVATPGL SSDPIALGVL QDKDLFSVFA DPNMLDTLVP 180

AHPALVNAIV LVLHSVAGSA PMPGTDSSSR SMPSSSYRDM PGGFLFEGLS DDEDDFHPNT 240

RSTPSSSTPS SRPASLGYSG AAGPRPITQS ELATALALAS TPESSSHTPT PGTQGHSSGT 300

SPMSSGVQSG TPITNDLFSQ ALQHALQASG QPSLQSQWQP QLQQLRDMGI QDDELSLRPC 360

RPPVGTSKQP WSSSLLEEPH ELPASPEPPA SCRGYCPWEA LMKVPPSLPS PIYLMVNSKK 420

KKKKKK 426

(SEQ ID NO:2)

Fig. 5

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GCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGGATGTCTC TCTCAGACTG     60
GCACCTGGCG GTGAAGCTGG CTGACCAGCC ACTTACTCCA AAGTCTATTC TTCGGTTGCC    120
AGAGACAGAA CTGGGAGAAT ACTCGCTAGG GGGCTATAGT ATTTCATTTC TGAAGCAGCT    180
TATTGCTGGC AAACTCCAGG AGTCTGTTCC AGACCCTGAG CTGATTGATC TGATCTACTG    240
TGGTCGGAAG CTAAAAGATG ACCAGACACT TGACTTCTAT GGCATTCAAC CTGGGTCCAC    300
TGTCCATGTT CTGCGAAAGT CCTGGCCTGA ACCTGATCAG AAACCGGAAC CTGTGGACAA    360
AGTGGCTGCC ATGAGAGAGT TCCGGGTGTT GCACACTGCC CTGCACAGCA GCTCCTCTTA    420
CAGGGAGGCG GTCTTTAAGA TGCTCAGCAA TAAGGAGTCT CTGGATCAGA TCATTGTGGC    480
CACCCCAGGC CTCAGCAGTG ACCCTATTGC TCTTGGGGTT CTCCAGGACA AGGACCTCTT    540
CTCTGTCTTC GCTGATCCCA ATATGCTTGA TACGTTGGTG CCTGCTCACC CAGCCCTCGT    600
CAATGCCATT GTCCTGGTTC TGCACTCCGT AGCAGGCAGT GCCCCAATGC CTGGGACTGA    660
CTCCTCTTCC CGGAGCATGC CCTCCAGCTC ATACCGGGAT ATGCCAGGTG GCTTCCTGTT    720
TGAAGGGCTC TCAGATGATG AGGATGACTT TCACCCAAAC ACCAGGTCCA CACCCTCTAG    780
CAGTACTCCC AGCTCCCGCC CAGCCTCCCT GGGGTACAGT GGAGCTGCTG GGCCCCGGCC    840
CATCACCCAG AGTGAGCTGG CCACCGCCTT GGCCCTGGCC AGCACTCCGG AGAGCAGCTC    900
TCACACACCG ACTCCTGGCA CCCAGGGTCA TTCCTCAGGG ACCTCACCAA TGTCCTCTGG    960
TGTCCAGTCA GGGACGCCCA TCACCAATGA TCTCTTCAGC CAAGCCCTAC AGCATGCCCT   1020
TCAGGCCTCT GGGCAGCCCA GCCTTCAGAG CCAGTGGCAG CCCCAGCTGC AGCAGCTACG   1080
TGACATGGGC ATCCAGGACG ATGAGCTGAG CCTGCGGCCC TGCAGGCCAC CGGTGGGGAC   1140
ATCCAAGCAG CCCTGGAGCT CATCTTTGCT GGAGGAGCCC CATGAACTCC CTGCTTCCCC   1200
TGAACCCCCA GCAAGTTGCA GAGGCTACTG CCCTTGGGAG GCACTCATGA AGGTGCCTCC   1260
ATCTCTCCCT GTC                                                      1273
```

Fig. 6

684

MSLSDWHLAV KLADQPLTPK SILRLPETEL GEYSLGGYSI SFLKQLIAGK LQESVPDPEL 60

IDLIYCGRKL KDDQTLDFYG IQPGSTVHVL RKSWPEPDQK PEPVDKVAAM REFRVLHTAL 120

HSSSSYREAV FKMLSNKESL DQIIVATPGL SSDPIALGVL QDKDLFSVFA DPNMLDTLVP 180

AHPALVNAIV LVLHSVAGSA PMPGTDSSSR SMPSSSYRDM PGGFLFEGLS DDEDDFHPNT 240

RSTPSSSTPS SRPASLGYSG AAGPRPITQS ELATALALAS TPESSSHTPT PGTQGHSSGT 300

SPMSSGVQSG TPITNDLFSQ ALQHALQASG QPSLQSQWQP QLQQLRDMGI QDDELSLRPC 360

RPPVGTSKQP WSSSLLEEPH ELPASPEPPA SCRGYCPWEA LMKVPPSLP 409

Fig. 7